

SEQUENCE LISTING

<110> Boehringer Ingelheim Pharma KG

<120> Method for identifying substances which positively influence inflammatory conditions

<130> 1/1179

<140>

<141>

<150> US 60/257,856

<151> 2000-12-22

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 1

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<210> 2

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 2

gtcgtcaaga tgctaccggt cagga 25

<210> 3

<211> 802

<212> DNA

<213> Homo sapiens

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tatatggaat ggatcctgaa ctccattagca tggtagcaag accagctcgt gcagttttac 180
ttctctttcc tattacagaa aagtatgaag tattcagaac agaaggaggaa gaaaaataaa 240
aatctcagggt acaagatggt acatcatcag tatatttcat gaagcaaaaca atcagcaaatg 300
cctgtggaac aattggactg attcatgcta ttgcaaaaca taaagacaag atgcactttg 360
aatctggatc aaccttgaaa aaattcctgg aggaatctgt gtcaatgagc cctgaagaac 420

gagccagata cctggagaac tatgatgcca tccgagttac tcatgagacc agtgcaccatg 480
 aaggtcagac tgaggcacca agtatagatg agaaagtaga tcttcatttt attgcattag 540
 ttcatgtaga tgggcatctc tatgaattag atgggcggaa gccatttcca attaaccatg 600
 gtgaaactag tgatgaaact ttatttagagg atgccataga agtttgcaag aagtttatgg 660
 agcgcgacc tgatgaaact agatttaatg cgattgctct tctgcagca tagcttgta 720
 ataatggaaa caccaaaaac tgtattattt gcaactaaat tttctctgcc catacactaa 780
 ctcaaaaatt ttgatatttt cc 802

<210> 4
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 4
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 1 5 10 15
 Asn Gln Phe Leu Lys Gln Leu Gly Leu His Pro Asn Trp Gln Phe Val
 20 25 30
 Asp Val Tyr Gly Met Asp Pro Glu Leu Leu Ser Met Val Pro Arg Pro
 35 40 45
 Val Cys Ala Val Leu Leu Leu Phe Pro Ile Thr Glu Lys Tyr Glu Val
 50 55 60
 Phe Arg Thr Glu Glu Glu Glu Lys Ile Lys Ser Gln Gly Gln Asp Val
 65 70 75 80
 Thr Ser Ser Val Tyr Phe Met Lys Gln Thr Ile Ser Asn Ala Cys Gly
 85 90 95
 Thr Ile Gly Leu Ile His Ala Ile Ala Asn Asn Lys Asp Lys Met His
 100 105 110
 Phe Glu Ser Gly Ser Thr Leu Lys Lys Phe Leu Glu Glu Ser Val Ser
 115 120 125
 Met Ser Pro Glu Glu Arg Ala Arg Tyr Leu Glu Asn Tyr Asp Ala Ile
 130 135 140
 Arg Val Thr His Glu Thr Ser Ala His Glu Gly Gln Thr Glu Ala Pro
 145 150 155 160
 Ser Ile Asp Glu Lys Val Asp Leu His Phe Ile Ala Leu Val His Val
 165 170 175
 Asp Gly His Leu Tyr Glu Leu Asp Gly Arg Lys Pro Phe Pro Ile Asn
 180 185 190
 His Gly Glu Thr Ser Asp Glu Thr Leu Leu Glu Asp Ala Ile Glu Val
 195 200 205
 Cys Lys Lys Phe Met Glu Arg Asp Pro Asp Glu Leu Arg Phe Asn Ala
 210 215 220

Ile Ala Leu Ser Ala Ala
225 230

<210> 5
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
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<210> 6
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
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<210> 7
<211> 866
<212> DNA
<213> Homo sapiens

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gcaaatgggtg tggattatgc aactgagaaa aaacagaaat ccattctgta tgatgagcga 180
agtgtacaca aagtagaacc aattaccaag catataggtt tgggtgtacag tggcatgggc 240
cccgaattaca gagtgccttg gcacagagct cgaaaactag ctcaacaata ctatcttctg 300
taccagaac ccattctctac agctcagctg gtacagagag tagcttctgt gatgcaagaa 360
tatactcagt caggtgggtg tcgtccattt ggagtttctt tacttatttg tggttggaat 420
gaggagcagc catatttatt tcagtcagat ccactctggag cttactttgc ctggaaaagct 480
acagcaatgg gaaagaacta tgtgaatggg aagactttcc ttgagaaaag atataatgaa 540
gatctggaac ttgaagatgc catcacaata gccatcttaa ccctaaagga aagctttgaa 600
gggcaaatga cagaggataa catagaagtt ggaatctgca atgaagctgg atttaggagg 660
cttactccaa ctgaagttaa ggattacttg gctgccatag cataacaatg aagtgaactga 720
aaaatccaga atttcagata atctatctac ttaaacatgt ttaaagtatg tttgttttg 780
cagacttttt gcatacttat ttctacatgg tttaaatcga ctgtttttaa aatgacactt 840
ataaatccca ataaactggt aaaccc 866

<210> 8
<211> 234
<212> PRT
<213> Homo sapiens

<400> 8

Met Ala Glu Arg Gly Tyr Ser Phe Ser Leu Thr Thr Phe Ser Pro Ser
 1 5 10 15
 Gly Lys Leu Val Gln Ile Glu Tyr Ala Leu Ala Ala Val Ala Gly Gly
 20 25 30
 Ala Pro Ser Val Gly Ile Lys Ala Ala Asn Gly Val Val Leu Ala Thr
 35 40 45
 Glu Lys Lys Gln Lys Ser Ile Leu Tyr Asp Glu Arg Ser Val His Lys
 50 55 60
 Val Glu Pro Ile Thr Lys His Ile Gly Leu Val Tyr Ser Gly Met Gly
 65 70 75 80
 Pro Asp Tyr Arg Val Leu Val His Arg Ala Arg Lys Leu Ala Gln Gln
 85 90 95
 Tyr Tyr Leu Val Tyr Gln Glu Pro Ile Pro Thr Ala Gln Leu Val Gln
 100 105 110
 Arg Val Ala Ser Val Met Gln Glu Tyr Thr Gln Ser Gly Gly Val Arg
 115 120 125
 Pro Phe Gly Val Ser Leu Leu Ile Cys Gly Trp Asn Glu Gly Arg Pro
 130 135 140
 Tyr Leu Phe Gln Ser Asp Pro Ser Gly Ala Tyr Phe Ala Trp Lys Ala
 145 150 155 160
 Thr Ala Met Gly Lys Asn Tyr Val Asn Gly Lys Thr Phe Leu Glu Lys
 165 170 175
 Arg Tyr Asn Glu Asp Leu Glu Leu Glu Asp Ala Ile His Thr Ala Ile
 180 185 190
 Leu Thr Leu Lys Glu Ser Phe Glu Gly Gln Met Thr Glu Asp Asn Ile
 195 200 205
 Glu Val Gly Ile Cys Asn Glu Ala Gly Phe Arg Arg Leu Thr Pro Thr
 210 215 220
 Glu Val Lys Asp Tyr Leu Ala Ala Ile Ala
 225 230